

Amendments to the Claims

Claim 1 (Currently amended): A method of identifying variation in a genotype of an animal, wherein said variation is associated with a phenotypic difference in meat quality traits of said animal, wherein said variation is a polymorphism characterized by an asparagine codon at an amino acid position analogous to amino acid 298 of a human MC4R gene product, wherein said animal with an asparagine codon at position 298 is indicative of said animal more likely to have favorable meat quality characteristics than an animal with an aspartic acid codon at position 298,
~~an animal which possesses a genotype indicative of a phenotypic trait,~~ said method comprising:
obtaining a nucleic acid sample from said animal; ~~and;~~
assaying for the presence of a polymorphism in a the MC4R gene of the said sample, or a
~~polymorphism linked thereto, said polymorphism being one which has been previously shown to be significantly associated with a phenotypic trait,~~ wherein said polymorphism at the amino acid level is characterized as a change from an aspartic acid codon to an asparagine codon at an amino acid position corresponding to amino acid 298 of a human MC4R gene product, wherein said animal with an asparagine codon is indicative of said animal more likely to have favorable meat quality characteristics such as pH, marbling, color and drip loss than an animal with an aspartic acid codon at position 298; and ,said
~~polymorphism further being an aspartic acid codon, wherein the aspartic acid codon is GAU, which is changed to an asparagine codon, wherein the asparagine codon is AAU at amino acid position analogous to amino acid 298 of the human MC4R gene; and~~
~~associating said animal with said phenotypic trait based upon the genotype present in said animal.~~
relating said polymorphism to said phenotype.

Claims 2-3 (Cancelled)

Claim 4 (Original): The method of claim 1 wherein the animal is a pig.

Claim 5 (Previously presented): The method of claim 1 wherein the step of assaying for the presence of the polymorphism is a method employing allele specific oligonucleotides.

Claim 6 (Previously presented): The method of claim 1 wherein said polymorphism is assayed by PCR amplification and restriction.

Claim 7 (Previously presented): The method of claim 1 wherein the step of assaying for the presence of the polymorphism employs a technique selected from the group consisting of restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), and use of linked genetic markers.

Claim 8 (Previously presented): The method of claim 7 wherein a step of assaying identifying the polymorphism comprises RFLP analysis.

Claim 9 (Currently amended): The method of claim 1 further comprising the step of: amplifying a region of the MC4R gene sequence or a region therein which contains said polymorphism.

Claim 10 (Currently amended): The method of claim 9 further comprising the step of digesting the amplified region with ~~the~~ a restriction endonuclease *Taq I*.

Claims 11-18 (Cancelled)

Claim 19 (Currently amended): The method of claim ~~1~~ 9 wherein ~~primers used in said an amplification are selected from a group consisting of SEQ ID NOS: 6 and 7, and wherein said polymorphism is at position 678 of the~~ amplification product produced by primers SEQ ID NO:5 and SEQ ID NO:6~~MC4R gene in the sample.~~

Claim 20 (Currently amended): A method of identifying an animal which possess a desired genotype indicative of a ~~significantly correlated~~ phenotypic trait, the method comprising: obtaining a nucleic acid sample from an animal, said sample comprising a seventh transmembrane region of an MC4R gene, ~~digesting the sample with a restriction enzyme that recognizes the same site as *Taq I* to obtain fragments,~~ separating the fragments obtained from the digestion, and identifying the presence or absence of a *Taq I* site in one allele of the MC4R gene, wherein the presence of a *Taq I* site ~~polymorphism~~ indicates that the animal possesses a desired genotype indicative of a significantly associated phenotypic trait selected from the group consisting of pH, marbling, color and drip loss.

Claim 21 (Currently amended): The method of claim 20 further comprising the step of selecting animals with a the desired genotype for breeding.

Claim 22 (Currently amended): The method of claim 20 further comprising: amplifying the nucleic acid sample with a forward primer and a reverse primer; digesting the amplified nucleic acid with a restriction enzyme such that nucleic acid fragments are generated; separating the nucleic acid fragments according to size such that a restriction fragment pattern is generated wherein the site polymorphism is identifiable ~~from~~ by a *Taq I* digestion pattern of an amplified product characterized by fragments of 466, 225, and 76 bp when a guanine is present at base 678 of the MC4R gene and fragments 542 and 225 bp when an adenine is present at base 678 of the amplified product ~~MC4R gene when a restriction enzyme which cuts at the same recognition site as *Taq I* is used.~~

Claim 23 (Currently amended): The method of claim ~~20~~ 22 wherein the restriction fragment pattern is characterized ~~site is identifiable from a *Taq I* digestion of a amplified product by~~ fragments of 156 and 70 bp when allele 1 of the MC4R gene is present and a fragment of 226 bp

when allele 2 of the MC4R gene is present, when a restriction enzyme that acts at the same recognition site as *Taq I* is used.

Claim 24 (Currently amended): The method of claim 20 wherein the animal is a pig~~step of identifying comprises:~~
~~detecting the Taq I site by amplification.~~

Claim 25 (Withdrawn): A kit for evaluating a nucleic acid sample from an animal comprising:
a reagent in a container that identifies a polymorphism in a MC4R gene.

Claim 26 (Withdrawn): The kit of claim 25 wherein the reagent is a primer that amplifies the MC4R gene or a fragment thereof.

Claim 27 (Withdrawn): The kit of claim 25 further comprising:
a DNA polymerase which cleaves the MC4R gene,
a forward primer, and
a reverse primer,
wherein the primers are capable of amplifying a region of the MC4R gene which contains a polymorphic site.

Claim 28 (Withdrawn): A primer for assaying the presence of a polymorphic Taq I site in the MC4R gene wherein the primer comprises a sequence selected from the group consisting of SEQ. ID NO:6, SEQ. ID NO:7, SEQ. ID NO:8, SEQ. ID NO:9, SEQ. ID NO:10, and SEQ. ID NO:11.

Claim 29 (Currently amended): A method for selecting animals for the desired traits of favorable meat quality comprising the steps of:
obtaining a nucleic acid sample from an animal,
identifying a polymorphism said polymorphism being a nucleotide substitution at position 678 of

SEQ ID NO:1, and
selecting the animals which have the nucleotide associated with ~~the~~ a desired trait traits selected from the group consisting of pH, marbling, color and drip loss at position 678, wherein the presence of the polymorphism indicates that the animal possesses a genotype
indicative of a favorable meat quality ~~which comprises~~ selected from the group consisting of pH, marbling, color, and drip loss.

Claim 30 (Currently amended): A method for indirect selection for a polymorphism in an MC4R gene comprising:
obtaining a nucleic acid sample from an animal, and
identifying a nucleotide substitution at position 678 of SEQ ID NO:1 with a DNA marker known to be associated with ~~the~~ MC4R gene, said DNA marker further being ~~one which is known to be~~ associated with meat quality, wherein specific alleles of the DNA marker are used to make the indirect identification of the nucleotide substitution, and
selecting said animals based upon the presence of nucleotide substitution.

Claim 31 (Original): The method of claim 30 wherein the linked marker is selected from the group consisting of S0331, BHT0433, and S0313.

Claim 32 (Currently amended): A method of identifying animals which possess a desired genotype indicative of favorable meat quality traits, the method comprising:
determining an association between a MC4R genotype and a trait of interest by obtaining a sample of animals from a line or breed of interest,
preparing a nucleic acid sample from each animal in the sample,
determining the genotype of the MC4R gene by screening for a polymorphism being a point mutation in the 7th transmembrane domain of the MC4R gene, wherein the presence of the polymorphism indicates that the animal possesses a genotype indicative of favorable meat quality ~~which comprises~~ characteristics selected from the group consisting of pH, marbling, color, and drip loss and
calculating the association between the MC4R genotype and the trait.

Claim 33 (Previously presented): A method of selecting animals which possess a desired MC4R genotype indicative of a significantly associated phenotypic trait, the method comprising: obtaining a nucleic acid sample from an animal by screening for a polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from the MC4R gene, identifying the genotype of the MC4R gene of the animal, and selecting those animals which have the genotype associated with the desired traits, wherein the presence of the polymorphism indicates that the animal possesses a genotype previously shown to be significantly associated with said desired trait.

Claim 34 (Currently amended): A method of determining the potential meat quality of an animal, said method comprising: obtaining a nucleic acid sample from said animal and then assaying for the presence of a polymorphism in the MC4R gene of the sample, said polymorphism being a G to A point mutation at position 678 of SEQ ID NO: 1 from the MC4R gene, said polymorphism being one which is associated with favorable meat quality characteristics ~~which comprises~~ selected from the group consisting of pH, marbling, color, and drip loss, wherein the presence of the polymorphism indicates that the animal possesses a genotype indicative of favorable meat quality.

Claim 35 (Currently amended): A method of selecting animals for breeding, said method comprising: obtaining a nucleic acid sample from said animal; assaying for the presence of a polymorphism in the MC4R gene of said sample, said polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from the MC4R gene, said polymorphism being ~~one which has previously been shown to be significantly~~ correlated with a phenotypic trait; and using the MC4R genotype as part of a selection model based on the estimated value of the effect of the marker genotype, and thereafter

selecting animals on the basis of this estimated value for use in breeding.

Claim 36 (Previously presented): A method of segregating animals in order to provide uniformity at slaughter comprising:
obtaining a nucleic acid sample from said animal; and
assaying for the presence of a polymorphism in the MC4R gene of said sample, said polymorphism being a G to A point mutation at position 678 of SEQ ID NO:1 from the MC4R gene, said polymorphism being one which is associated with meat quality, segregating said animals based upon the polymorphism present in said animal.

Claim 37 (Currently amended): A method for selecting animals for breeding, said method comprising:
obtaining a nucleic acid sample from said animal;
assaying for the presence of a polymorphism in the seventh transmembrane domain of the MC4R gene of said sample said polymorphism being one which ~~is~~ ~~has been shown to be~~ significantly statistically associated with a phenotypic trait; and
selecting animals with a favorable allele for inclusion in breeding stock.

Claim 38 (Cancelled)

Claim 39 (Cancelled)

Claim 40 (Currently amended): A method for selecting pigs for the desired trait of improved meat quality comprising the steps of:
obtaining a nucleic acid sample from a pig,
screening ~~the said pig~~ for a polymorphism comprising a G to A mutation at position analogous to position 678 of SEQ ID NO:1 from the MC4R gene, said polymorphism being one which is significantly associated with a favorable meat quality characteristic, and
selecting ~~the pigs~~ said pig which have the nucleotide associated with the desired traits at position 678.